In the claims:

1. (Original) An isolated nucleic acid molecule comprising the sequence of SEQ ID NO: 1.

2. (Currently amended) An isolated nucleic acid molecule comprising a sequence fully complementary to the sequence of claim 1.

3. (Original) A vector comprising the isolated nucleic acid molecule of claim 1, operably linked to a reporter gene.

4. (Original) The vector according to claim 3, wherein said reporter gene sequence encodes luciferase.

5. (Original) A host cell comprising the vector of claim 3.

6. (Withdrawn) A method for detection of a single nucleotide polymorphism (SNP) in the FGF-3 gene in a mammal, which method comprises: a) isolating a nucleic acid sample from said mammal; and b) determining whether a cytosine or thymine is present at position 69 of SEQ ID NO: 1.

7. (Withdrawn) The method according to claim 6, wherein the mammal is a human.

8. (Withdrawn) The method according to claim 6, wherein the determination of the presence of a cytosine or thymine comprises amplifying a reference portion of the mammal's genome.

9. (Withdrawn) The method according to claim 8, wherein the reference portion is amplified using a pair of primers

consisting essentially of nucleotide sequences of SEQ ID NO: 4 and SEQ ID NO: 5.

10. (Withdrawn) The method according to claim 8, wherein the reference portion comprises the 5' untranslated region of FGF-3 gene.

11. (Withdrawn) The method according to claim 10, wherein the 5' untranslated region of FGF-3 gene comprises the nucleotide residue located at position 69 of SEQ ID NO: 1.

12. (Withdrawn) The method according to 8, further comprising annealing a first oligonucleotide probe with a target portion of the mammal's genome prior to amplifying the reference portion, wherein the target portion includes the nucleotide residue located at position 69 of SEQ ID NO: 1.

13. (Withdrawn) The method according to claim 12, wherein the first probe comprises a flourescent label.

14. (Withdrawn) The method according to claim 13, wherein the fluorescent label is selected from FAM, TET, rhodamine, VIC, JOE, and HEX.

15. (Withdrawn) The method according to claim 13, wherein the first probe further comprises a fluorescence quencher.

16. (Withdrawn) The method according to claim 15, wherein the quencher is selected from TAMRA and DABCYL.

17. (Withdrawn) The method according to claim 12, wherein the first probe consists essentially of the nucleotide sequence of

SEQ ID NO: 6.

18. (Withdrawn) The method according to claim 15, wherein the reference portion is amplified using a DNA polymerase having 5'→ 3' exonuclease activity.

19. (Withdrawn) The method according to claim 12, further comprising annealing a second oligonucleotide probe with said target portion of the mammal's genome prior to amplifying the reference portion, wherein said first probe is completely complimentary to the target portion of T-allele FGF-3 gene and said second probe is completely complimentary to the target portion of C-allele FGF-3 gene.

20. (Withdrawn) The method according to claim 19, wherein said second probe consists essentially of the nucleotide sequence of SEQ ID NO: 7.

21. (Withdrawn) The method according to claim 19, wherein said first probe comprises a first fluorescence label and said second probe comprises a second fluorescence label, said first and second fluorescence labels being detectably different.

22. (Withdrawn) The method according to claim 21, wherein said first and second fluorescence labels are selected from the group consisting of FAM, TET, rhodamine, VIC, JOE, and HEX.

23. (Withdrawn) The method according to claim 21, wherein said first and second probes further comprises a first and second fluorescence quencher, respectively.

24. (Withdrawn) The method according to claim 23, wherein said

first and second fluorescence quenchers are selected from the group consisting of TAMRA and DABCYL.

25. (Currently amended) A kit for identifying a polymorphism in SEQ ID NO: 1 of claim 1, ~~performing the method according to claim 6~~ comprising: a) a first oligonucleotide probe selected from the group consisting of SEQ ID NOS: 6 and 7, which anneals specifically with a target portion of the ~~mammal's~~ human genome, wherein said first probe comprises a first fluorescent label and a first fluorescence quencher attached to separate nucleotide residues thereof and said target portion includes the nucleotide residue located at position 69 of SEQ ID NO: 1; and b) a pair of primers for amplifying a reference portion of the FGF-3 gene, wherein said reference portion includes the nucleotide residue located at position 69 of SEQ ID NO: 1 and said primers are selected from the group consisting of SEQ ID NOS: 4 and 5.

26. (Original) The kit according to claim 25 further comprising a DNA polymerase having 5'→ 3' exonuclease activity.

27. (Original) The kit according to claim 26, further comprising a second oligonucleotide probe, wherein said first probe is completely complementary to said target portion if the nucleotide residue located at position 69 of SEQ ID NO: 1 is cytosine, and said second oligonucleotide probe is completely complementary to said target portion if the nucleotide residue located at position 69 of SEQ ID NO: 1 is thymine.

28. (Original) The kit according to claim 27 further comprising an instructional material.

29. (Withdrawn) A method of assessing the relative

susceptibility of a mammal to cancer, said method comprising the detection of the SNP in FGF-3 gene according to claim 6, wherein if the mammal comprises nucleotide cytosine at position 69 of SEQ ID NO: 1, then the mammal has a greater susceptibility to the cancer than a mammal of the same type which does not comprise nucleotide cytosine at position 69 of SEQ ID NO: 1.

30. (Withdrawn) The method according to claim 29, wherein said the mammal is a human.

31. (Withdrawn) The method according to claim 30, wherein the cancer is selected from the group consisting of esophageal, breast, ovarian, prostate, and head and neck cancer.

32. (Withdrawn) The method according to claim 31, wherein the esophageal cancer is esophageal squamous cell carcinoma.

33. (Currently amended) A microarray having at least one oligonucleotide probe that can anneal with a target portion of a ~~mammal's~~ human genome, wherein the target portion includes the nucleotide residue located at position 69 of SEQ ID NO: 1 and is selected from the group consisting of SEQ ID NOS: 6 and 7.

34. (Cancelled)